

# **EXHIBIT I**

**CONFIDENTIAL**



## Houston Forensic Science Center

### Forensic Biology Division

500 Jefferson St, 13<sup>th</sup> Floor, Houston, Texas 77002  
(713) 929-6760



**Agency Case Number:** 112736620  
**Forensic Case Number:** 2020-11551

**Report Date:** March 31, 2022  
**Requestor Information:** Houston Police Department  
1200 Travis Houston, TX, 77002

### Laboratory Report #2

**Offense:** Aggravated Assault (HPD Officer)      **Previous Analysis:** Previous analysis has been conducted on this case.

### ITEMS OF EVIDENCE:

- 15.1.1      Portion of "Poss. contact DNA from EM3" swab
- 15.2.1      Portion of "Poss. contact DNA from cartridges EM3" swab
- 43.2.1      Portion of bloodstain card from Julius Kehyei (ML20-3635)

### SCREENING RESULTS AND INTERPRETATIONS:

#### **Item 15.1.1 (Portion of "Poss. contact DNA from EM3" swab)**

The detection of human DNA was positive on this item. This item was processed further.

#### **Item 15.2.1 (Portion of "Poss. contact DNA from cartridges EM3" swab)**

The reagent blank associated with this item was contaminated; therefore, it did not meet quality assurance standards. No results will be reported for this item. Please contact the analyst for more information. See Quality Report 2020-097.

**CONFIDENTIAL**

Incident Number: 112736620

Houston Forensic Science Center

Forensic Case Number: 2020-11551 (2)

Report Date: March 31, 2022

**DNA RESULTS AND INTERPRETATIONS:****Item 15.1.1 (Portion of "Poss. contact DNA from EM3" swab)**

The male DNA profile from this item was interpreted as a single-source profile.

The DNA results are approximately 16.7 octillion times more likely if they originated from Julius Kehyei than if they originated from an unknown, unrelated individual. This provides very strong support that Julius Kehyei is a contributor to the DNA from this item.

**Item 15.2.1 (Portion of "Poss. contact DNA from cartridges EM3" swab)**

The reagent blank associated with this item was contaminated; therefore, it did not meet quality assurance standards. No results will be reported for this item. Please contact the analyst for more information. See Quality Report 2020-097.

**Item 43.2.1 (Portion of bloodstain card from Julius Kehyei (ML20-3635))**

A single-source male DNA profile was obtained from this item.

**NOTES:**

The eligible DNA profile from Item 43.2.1 has been entered into CODIS.

1. Presumptive tests are only an indication of the presence of a biological fluid, such as blood or semen, which means material other than blood or semen can also give a positive result. The phenolphthalein test and the alternate light source are used to presumptively test for the presence of blood. The alternate light source, the acid phosphatase test, and the Seratec® PSA Semiquant test are used to presumptively test for the presence of semen.
2. Items screened for the presence of blood may be confirmed using the ABACard® HemaTrace® test which is a qualitative detection method specifically designed for forensic identification of human blood. Hemoglobin from the Family Mustelidae (ferrets) and higher primates may also give a positive result.
3. Items screened for the presence of semen may be further tested using the Seratec® PSA Semiquant test for the presence of prostate specific antigen (PSA). PSA can be detected in seminal fluid without spermatozoa (e.g., seminal fluid of vasectomized males). However, PSA is also now known to be found at very low levels in different tissues and fluids such as breast tissue and tumors, periurethral glands, breast milk, amniotic fluid, and female urine.
4. Items screened for the presence of semen may be confirmed through microscopic examination which is used to visualize human spermatozoa cells.
5. Items screened for autosomal and male DNA were extracted and then tested using real-time PCR amplification, detection, and quantification. The Quantifiler® Trio kit uses three human-specific target loci: Small Autosomal, Large Autosomal, and a Y-chromosome target. Each consists of multiple copies dispersed on various autosomal chromosomes (Small Autosomal and Large Autosomal) or multiple copies on the Y-chromosome.
6. The "detection of male/human DNA was insufficient" indicates that the amount of male/human DNA detected is above 0.000 ng/µl but below the minimum interpretation threshold of 0.001 ng/µl.
7. The "male DNA was in a significantly lower proportion to the total human DNA" indicates that the amount of male DNA detected is above the minimum interpretation threshold of 0.001 ng/µl, however it is potentially overshadowed by a significantly higher amount of female DNA. This item may be suitable for Y-STR analysis if consensual sex partner(s) and/or suspect known samples are made available for testing.

**CONFIDENTIAL****Incident Number:** 112736620**Houston Forensic Science Center****Forensic Case Number:** 2020-11551 (2)**Report Date:** March 31, 2022

8. In cases where a single assailant is indicated and no consensual sex partner within 48 hours of the exam is specified (per the sexual assault kit medical report) not all items positive for male DNA will be taken forward initially. Please contact the lab if further testing is required in this case.
9. The items taken forward to DNA analysis were amplified using polymerase chain reaction (PCR). The following STR loci were analyzed: D3S1358, vWA, D16S539, CSF1PO, TPOX, D8S1179, D21S11, D18S51, DYS391, D2S441, D19S433, TH01, FGA, D22S1045, D5S818, D13S317, D7S820, SE33, D10S1248, D1S1656, D12S391, and D2S1338, along with gender determining markers Amelogenin and a Y indel.
10. For items in which male DNA was detected on an item and no comparison/interpretation was made, Y-STR analysis may be possible if consensual sex partner(s) and/or suspect known samples are made available for testing. Please contact the laboratory for further information.
11. When a differential extraction is performed, Fraction 1 refers to the extract designed to isolate sperm DNA, if present (previously referred to as the sperm fraction) and Fraction 2 refers to the extract designed to isolate non-sperm DNA, if present (previously referred to as the epithelial fraction).
12. STRmix™ is a fully continuous probabilistic genotyping forensic software which combines biological modeling with mathematical processes in order to (1) interpret and attempt to deconvolute DNA profiles in the presence or absence of conditioned samples, and (2) compare reference samples (comparison samples) to evidence samples and provide statistical weight in the form of a likelihood ratio (LR).
13. The LR is a statistic that considers the probability of obtaining the evidence given two competing explanations, Hypothesis 1 and Hypothesis 2. The LR reported is a lower bound highest posterior density (HPD) which is a conservative estimate of the LR. The LR reported is the lowest LR for the African American, Asian, Caucasian, or Hispanic populations, using allele frequencies taken from the revised "U.S. population data for 29 autosomal STR loci." Forensic Sci. Int. Genet. 7: e82-e83 and Forensic Sci. Int. Genet. 31: e36-e40.
14. Verbal scale used for likelihood ratio statistical results:

Likelihood ratios occur on a continuum, as likelihood ratios increase in magnitude the verbal scale reflects stronger degrees of support. The categories defined in the verbal scale below were chosen in part based on the observation that adventitious support for a proposition is most commonly observed within the Limited Support category and generally not expected within the Very Strong Support category. Adventitious support occurs when a known non-contributor to a sample generates a LR in support of their inclusion or a known contributor to a sample generates a LR in support of their exclusion. The largest LR of a known non-contributor generated during the laboratory validation was 230.

Hypothesis 2					Hypothesis 1					
Increasing support in favor of H2					Increasing support in favor of H1					
Excluded	Very Strong Support	Strong Support	Moderate Support	Limited Support	Uninformative	Limited Support	Moderate Support	Strong Support	Very Strong Support	Assumed
	≥1,000,000	10,000 - <1,000,000	100 - <10,000	2 - <100	0.5 - <2	2 - <100	100 - <10,000	<1,000,000	≥1,000,000	

*Recommendations of the SWGDAM Ad Hoc Working Group on Genotyping Results Reported as Likelihood Ratios (July 12, 2018)*

15. The LRs referenced in this report are based upon a range of propositions that can explain the evidence. Either interested party to this case, prosecution and/or defense, may request an additional likelihood ratio that maintain the number of contributors listed in the report. All requests must be submitted in a timely manner, must be reasonable given the test results, and must be within the capability and validated application of the program used.
16. All DNA extracts are being retained in the laboratory. Any other items will be returned to the submitting agency.
17. Laboratory activities described in this report that were conducted by the Forensic Biology Division prior to October 4, 2019 were conducted at 1200 Travis Street, Houston, TX 77002.



Rebecca C Gonzales  
Assistant CODIS Administrator

**CONFIDENTIAL**

**Incident Number:** 112736620

**Houston Forensic Science Center**

**Forensic Case Number:** 2020-11551 (2)

**Report Date:** March 31, 2022

Assigned Analyst

If evidence is accepted for analysis, HFSC assumes no responsibility for the investigative information, collection, sampling or description of evidentiary samples (denoted in quotation marks) prior to submission to the laboratory, nor in the association of these items to individuals when provided by the submitting agency. The only exception to this statement is for evidentiary samples handled by HFSC staff members at the time of collection. This disclaimer does not apply to item descriptions created before this disclaimer became effective, March 15, 2022.

The prosecutor and defense counsel may obtain additional documents related to this case by submitting a request to [Triage@HoustonForensicScience.org](mailto:Triage@HoustonForensicScience.org). Requests should state the requestor's connection to the case and include full contact information.